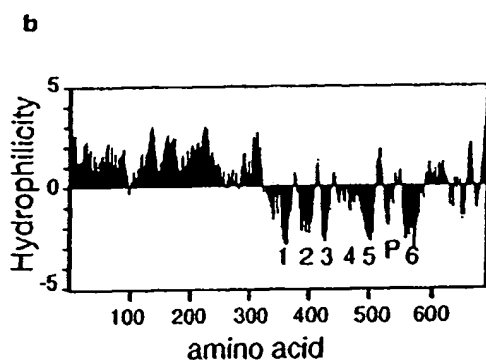


a

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MDQSSRRDES YHETHPGSLDPSHQSHPHPHPTLHRPNQGGVYYDSPQH 50
GMFQQPYQQHGGFHQQNELQHLREFSDSHDNAFSHHSYQQDRAGVSTLPN 100
NISHAYGGSHPLAESQHSQSGPRIDPNHHPHQDDPHRPSEPLSHPS 150
TGSHQGTTHQQYHERSHHLNPQQNRDHADTISYRSSTRFYRSHAPFSRQE 200
RPHLHADHHHEGHHASHHGEHPHHKEQRHYHGDHMHIIHHRSPSASQL 250
SEGEDHVQKRKKAQRAHKAHTGNIFQLLWEKISHLLLGLQQMILSLTQS 350
      S1                                     S2
LGFETFIFIVVCLNTVILVAQTFTELEIRGEWYFMVLDSIFLSIYVLEAV 400
      S3
LKLIALGLEIFYDPWNNLDEFFIMVMAVLDFVLLQINSISYSFYNHSLFRI 450
      S4                                     S5
LKVFKSMRALRAIRVLRLSILTSLEHVAGTSLSGSLPSITAILTLMFTCL 500
      P
FLFSVVLRALFQDSDPKRFQNIFFTTLFTLFTMLTLDDWSLIYIDNRAQGA 550
      S6
WYIIIPILMIYIVIQYFIFLNLVIAVLVDNFQMAALLKGLEKVKLEQAARVH 600
EKLLDDSLTDLNKADANAQMTEEALKMQLIEGMFGNMTVKQRVLHFQFLQ 650
LVAAVEQHQQKFRSQAYVIDELVDMAFEAGDDDYGK 686

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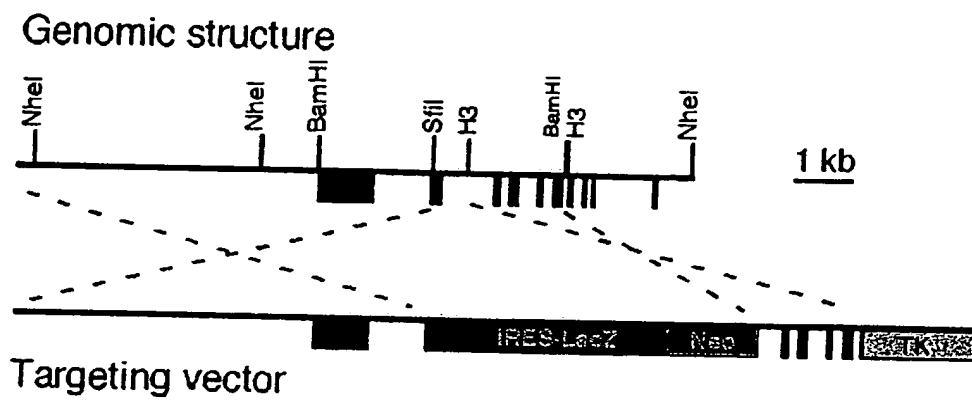


c

Pore region

CatSper	RFQNIFFTTLFTLFTMLTLDDWSLIYID
Cav1.2	NFDNFAFAMLTVFQCITMGQTDVLYN
I Cav2.2	NFDNLFAILTVFQCITMGQTDILYN
Cav3.1	NFDNIGYAWIAIFQVITLGGVDIMYF
Cav1.2	TFDNFPQSLLTVFQILTGGDNISVMYD
II Cav2.2	NFDTFPAAILTVFQILTGGDNIAVMYN
Cav3.1	NFDSLLWAIWTVFQILTGGDNKVLYN
Cav1.2	DFDNVLAAMMALETVSTFGCPPELLYR
III Cav2.2	HYDNVLWALLTLFTVSTFGCPHYLKH
Cav3.1	NFDNLGQALMSLFVLASKGCHVDIMYD
Cav1.2	NFQTFPQAVLLLPKCATGEAODIMLA
IV Cav2.2	NFRTFLQALMLLFRSATGEAHEIMLS
Cav3.1	TFRNFGMAFLTFRVSTGEAINGIMKO

FIG. 1

**FIG. 2**

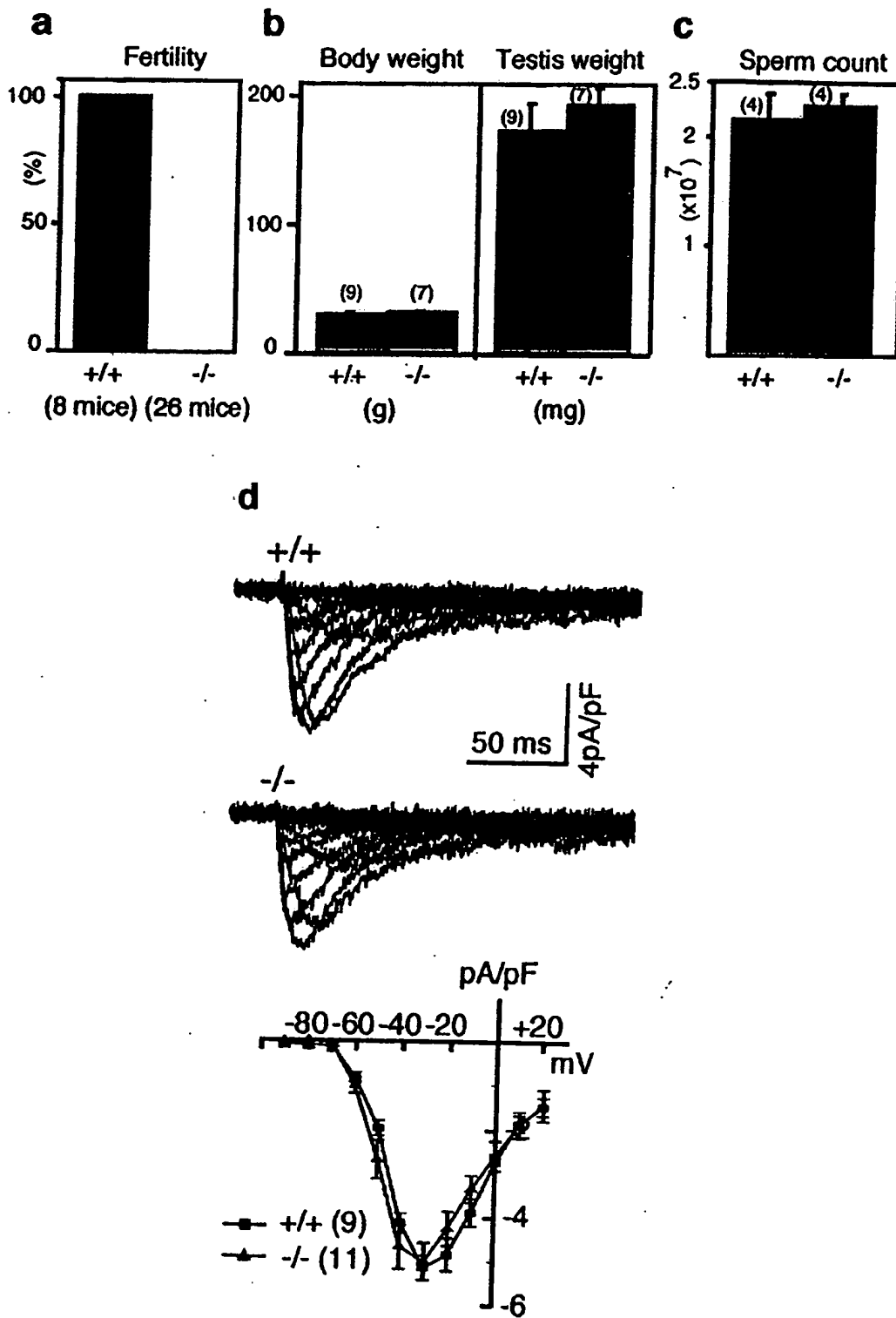
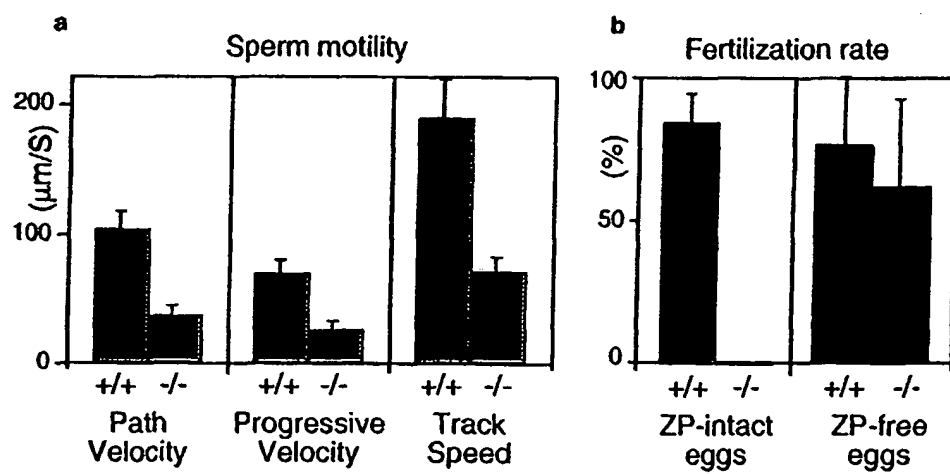


FIG. 3

**FIG. 4**

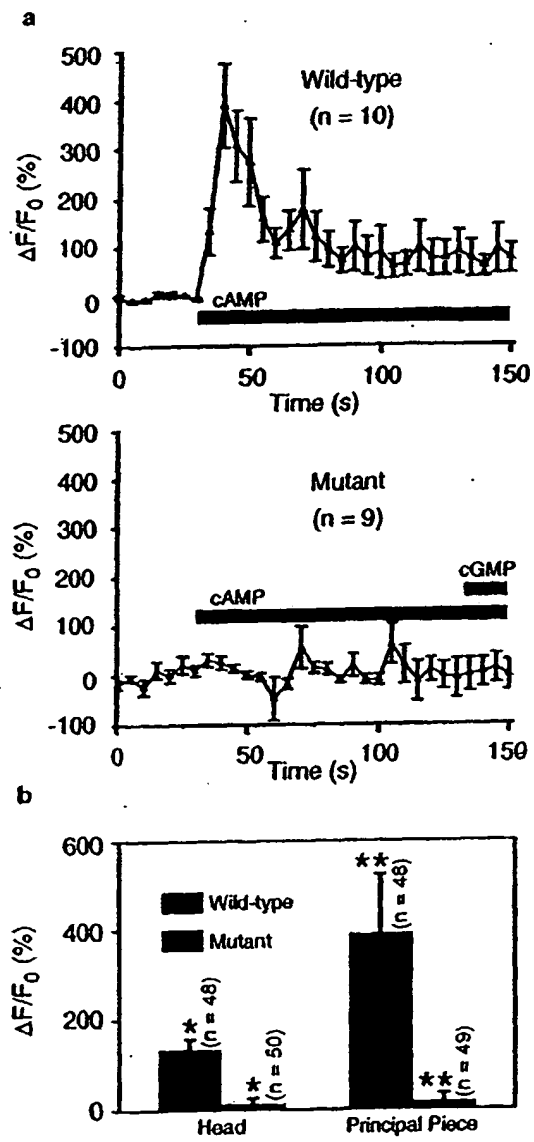


FIG. 5